

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/563,655
Source: IFWP
Date Processed by STIC: 1/18/06

ENTERED



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/563,655

DATE: 01/18/2006

TIME: 15:21:28

Input Set : A:\54-000410US.ST25.txt
 Output Set: N:\CRF4\01182006\J563655.raw

3 <110> APPLICANT: The Scripps Research Institute
 4 Anderson, J C
 5 Schultz, Peter G
 7 <120> TITLE OF INVENTION: COMPOSITIONS OF ORTHOGONAL LEUCYL-tRNA AND AMINOACYL-tRNA
 8 SYNTHETASE PAIRS AND USES THEREOF
 10 <130> FILE REFERENCE: 54-000410PC
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/563,655
 C--> 13 <141> CURRENT FILING DATE: 2006-01-05
 15 <160> NUMBER OF SEQ ID NOS: 72
 17 <170> SOFTWARE: PatentIn version 3.2
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 88
 21 <212> TYPE: DNA
 22 <213> ORGANISM: artificial
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: mutant tRNA
 27 <400> SEQUENCE: 1
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 30 gagggttcga atcccttccc tcgcacca 88
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 34 <211> LENGTH: 88
 35 <212> TYPE: DNA
 36 <213> ORGANISM: artificial
 38 <220> FEATURE:
 39 <223> OTHER INFORMATION: mutant tRNA
 41 <400> SEQUENCE: 2
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 44 gagggttcga atcccttccc tcgcacca 88
 47 <210> SEQ ID NO: 3
 48 <211> LENGTH: 88
 49 <212> TYPE: DNA
 50 <213> ORGANISM: artificial
 52 <220> FEATURE:
 53 <223> OTHER INFORMATION: mutant tRNA
 55 <400> SEQUENCE: 3
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 58 gagggttcga atcccttccc tggcacca 88
 61 <210> SEQ ID NO: 4
 62 <211> LENGTH: 89
 63 <212> TYPE: DNA
 64 <213> ORGANISM: artificial
 66 <220> FEATURE:
 67 <223> OTHER INFORMATION: mutant tRNA

P.6

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69 <400> SEQUENCE: 4
 70 gcgagggttag ccaagctcgg ccaacggcga cggaacttcct aatccgttct cgtaggagtt 60
 72 cgagggttcg aatcccttcc ctcgcacca 89
 75 <210> SEQ ID NO: 5
 76 <211> LENGTH: 89
 77 <212> TYPE: DNA
 78 <213> ORGANISM: artificial
 80 <220> FEATURE:
 81 <223> OTHER INFORMATION: mutant tRNA
 83 <400> SEQUENCE: 5
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 86 cgagggttcg aatccctccc ctcgcacca 89
 89 <210> SEQ ID NO: 6
 90 <211> LENGTH: 89
 91 <212> TYPE: DNA
 92 <213> ORGANISM: artificial
 94 <220> FEATURE:
 95 <223> OTHER INFORMATION: mutant tRNA
 97 <400> SEQUENCE: 6
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 104 <211> LENGTH: 88
 105 <212> TYPE: DNA
 106 <213> ORGANISM: artificial
 108 <220> FEATURE:
 109 <223> OTHER INFORMATION: mutant tRNA
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 118 <211> LENGTH: 77
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 120 <213> ORGANISM: artificial
 122 <220> FEATURE:
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 128 tccggccgc cggacca 77
 131 <210> SEQ ID NO: 9
 132 <211> LENGTH: 90
 133 <212> TYPE: DNA
 134 <213> ORGANISM: Escherichia coli
 136 <400> SEQUENCE: 9
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 139 ccgggggttc aaatccccct ctctccgcacca 90
 142 <210> SEQ ID NO: 10
 143 <211> LENGTH: 91
 144 <212> TYPE: DNA

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 148 <223> OTHER INFORMATION: mutant tRNA
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 157 <211> LENGTH: 88
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 159 <213> ORGANISM: Halobacterium sp. NRC-1
 161 <400> SEQUENCE: 11
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 164 gaggguucga aucccuuccc ucgcacca 88
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 170 <213> ORGANISM: artificial
 172 <220> FEATURE:
 173 <223> OTHER INFORMATION: consensus tRNA
 175 <400> SEQUENCE: 12
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 178 cggggguuca aauccccgccc cccgcacca 89
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 182 <211> LENGTH: 2799
 183 <212> TYPE: DNA
 184 <213> ORGANISM: Archaeoglobus fulgidus
 186 <400> SEQUENCE: 13
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 189 tttgagtccg atcctaattga gaaggagaag tttttctca caattcccta tccttacctt 120
 191 aatggaaatc ttacacgcagg tcacacgaga accttcacaa ttggcgatgc ctgcgcaga 180
 193 tacatgagaa tgaagggtca caacgttctc ttcccctcg gctttcatgt tacgggcacc 240
 195 ccaatcattg gccttgcgga gctcatagcc aagaggacg agaggacat agaggttac 300
 197 accaaataacc atgacgttcc gctggaggac ttgottcage tcacaactcc agagaaaatc 360
 199 gttgagtaact tctcaaggga ggcgctgcag gcttgaaga gcataggcta ctccattgac 420
 201 tggaggaggg tttcaccac aaccgatgaa gatgtatcaga gattcatcga gtggcagttac 480
 203 tggaaagctca aggagcttgg cctgattgtg aaggcacc 480
 205 cacgaccaga atccttgta agaccacgac cttotcgctg gggaggaggc aactattgtt 600
 207 gaatttaccc ttataaaagtt caggcttgaat gatggagacc tcattttccc ctgtgcaact 660
 209 ctccgtcccg aaaccgtgtt tggcgtcagc aacatctggg taaagccgac aacctacgta 720
 211 attgccgagg tggatgggaa aaagtggttt gtgagcaag aggcttacga gaagctcacc 780
 213 tacacggaga aaaaagtccg gctgctggag gaggttgatg cgtcgactt cttcggcaag 840
 215 tacgtcatag tcccgttgtt aaacagaaaa gtgcacattc tgcctgcaga gtttggatgac 900
 217 accgacaacg caacaggagt tgtgtatgac gttcccgac acgctccctt tgacctggct 960
 219 gccattgagg acttgaagag agacgaggaa acgtggcga agtacgaaat tgacaaaagc 1020
 221 gttgttagaga gcataaaagcc aatagttctg attaagacgg acattgaagg tggatggatgct 1080
 223 gagaagctaa taagagagct tggagtgaag agccagaagg acaaggagct gctggataag 1140
 225 gcaaccaaga ccctotacaa gaaggagtag cacacgggaa tcatgctgga caacacgatg 1200
 227 aactatgctg gaatgaaagt ttctgaggcg aaggagagag ttcatgagga tttggatgaa 1260
 229 cttggcttgg gggatgtttt ctacgagttc agcgagaagc ccgtaatctg caggtgcgg 1320

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231	acgaagtgcg	ttgttaaggt	tgttagggac	cagtggttcc	tgaactactc	caacagagag	1380
233	tggaaggaga	aggttctgaa	tcaccttcaa	aagatgcgaa	tcatccccga	ctactacaag	1440
235	gaggagttca	ggaacaagat	tgagtggctc	agggacaagg	cttgcgcag	aaggaagggg	1500
237	cttggAACGA	gaattccgtg	ggataaggag	tggctcatcg	agagccttc	agactcaaca	1560
239	atctacatgg	cctactacat	ccttgc当地	tacatcaacg	caggattgct	caaggccgag	1620
241	aacatgactc	ccgagttcct	cgactacgtg	ctgctggca	aaggtgaggt	tggaaaagtt	1680
243	gcggaaagctt	caaaaactcag	cgtggaggtt	atccagcaga	tcagggacga	cttcgagttac	1740
245	tggtatccc	ttgacctaag	aagcagtggc	aaggacttgg	ttgcaaacc	cctgctttc	1800
247	tacctcttcc	accacgtcgc	cattttcccg	ccagataagt	ggccgagggc	aattgccgt	1860
249	aacggatacg	tcagccttga	ggcaagaag	atgagcaaga	gcaaaaggcc	cttgcttaacg	1920
251	atgaagaggg	cggtgcagca	gtatggtgcg	gatgtgacga	ggctctacat	cctccacgct	1980
253	gcagagtacg	acagcgtatgc	ggacttggaa	agcagagagg	ttgaagggt	tgcaaaaccac	2040
255	ctcaggaggt	tctacaac	cgtgaaggag	aactacctga	aagaggtggg	agagctaaca	2100
257	accctcgacc	gctggcttgc	gagcaggatg	cagaggc	taaaggaagt	gaggaggct	2160
259	atggacaacc	tcagacgag	gagggccgtg	aatgcgcct	tcttcgagct	catgaacgac	2220
261	gtgagatgg	atctgaggag	aggaggtgag	aacctcgct	taatacttgg	cgactggatc	2280
263	aagctctcg	cccccttgc	tccgcacatt	tgcgaggagc	tgtggactt	gaagcatgac	2340
265	agctacgtca	gcctcgaaag	ctacccagaa	tacgacgaaa	ccagggttga	cgaggaggcg	2400
267	gagagaattt	aggaataacct	ccgaaacctt	tttgaggaca	ttcaggaaat	caagaagttt	2460
269	tttagcgatg	cgaaggaggt	ttacatttgc	cccgccgaag	actgaaagg	taaggcagca	2520
271	aaggtcg	ctgaaagcgg	ggatgttgg	gaggcgt	agcagctt	gcaggacgag	2580
273	gagcttagga	agctcggcaa	agaagtgtca	aatttgcgt	agaagat	caaagacaga	2640
275	aagaagctga	tgctagttaa	ggagtggaa	gttctgcagc	agaacctgaa	atttatttgg	2700
277	aatgagaccg	gactgaaggt	tattcttgc	actcagagag	ttccctgagga	gaagaggagg	2760
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285	<213>	ORGANISM:	Methanobacterium thermoautotrophicum				
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290	cctgtatgaca	gagaaaaagat	attcctcaca	gtcgcttacc	cctacc	tggcgatg	120
292	cacataggac	acgggaggac	ctacactgtc	cctgtatgtct	atgcacgg	caagaggatg	180
294	caggcgtaca	acgtcctgtt	tccatggcc	tggcatgtca	caggggcccc	tgtcataggg	240
296	atagcgcgga	ggattcagag	gaaggatccc	tggaccctca	aaatctacag	ggaggtccac	300
298	agggtcccc	aggatgagct	tgaacgttcc	agtgaccctg	agtacatagt	tgaataacttc	360
300	agcagggaaat	accggctgt	tatggaggat	atggctact	ccatcgact	gaggcgt	420
302	ttcaaaaacca	cggtatcccac	ctacagcagg	ttcatacgt	ggcagataag	gaagctgagg	480
304	gaccttggcc	tcgtaaggaa	gggcgc	cctgttaagt	actgcctg	atgtaaaaac	540
306	cctgtgggt	accatgac	ccttgagg	gagggggtt	ccataaa	acc	600
308	ctcaaaattca	aacttggaga	ctcatacct	gtcgaccca	ccttcagg	ccgagacaatc	660
310	tatggggcca	ccaaacctct	gctgaacc	gatgaggatt	atgtgagg	tgaacacaggt	720
312	gggtgaggag	ggataataag	caggcgt	gtggataatc	tttcacacca	gaaactggac	780
314	ctcaagg	tttccgtacgt	caaccc	ggatgtat	ggatgtgcgt	ggagaatcct	840
316	gtgacggcc	aggaacacccc	catactcc	gcttc	ttgacc	atatgccaca	900
318	gggttgtgt	tctctgtccc	tgcacatg	cctgcagact	tcatagcc	tgaggac	960
320	aggacagacc	atgaactcct	tgaaagg	gttctgagg	atgtgg	tgc	1020
322	cccgtaatg	tcatagcgt	ggatggctac	ggtgagttcc	cgccggccg	ggttatagag	1080
324	aaatttgg	tcagaaacca	ggaggacccc	cgccttgagg	atgc	cacccgg	1140

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326	aagatcgagc	atgcgagggg	tgttatgagc	agccacatcc	ctgtctatgg	tggtatgaag	1200										
328	gtctctgagg	cccgtaggt	catcgctgat	gaactgaagg	accaggccct	tgcagatgag	1260										
330	atgttatgaat	tcgctgagcg	acctgttata	tgccgctgcg	gtggcaggtg	cgttgtgagg	1320										
332	gtcatggagg	accagtggtt	catgaagtac	tctgatgacg	cctggaagga	cctcgcccac	1380										
334	aggtgcctcg	atggcatgaa	gataataccc	gaggaggtcc	gggccaactt	tgaataactac	1440										
336	atcgactggc	tcaatgactg	ggcatgttca	aggaggatag	gccttggAAC	aaggctgccc	1500										
338	tgggatgaga	ggtggatcat	cgaacccctc	acagactcaa	caatctacat	ggcatattac	1560										
340	accatcgcac	accgcctcag	ggagatggat	gccggggaga	tggacgatga	gttctttgat	1620										
342	gccatattcc	tagatgattc	aggaacctt	gaggatctca	gggaggaatt	ccggtaactgg	1680										
344	taccccttg	actggaggct	ctctgaaag	gacctcatag	gcaatcacct	gacattccat	1740										
346	atattccacc	actcagccat	atccctgag	tcagggtgcc	cccggggggc	tgtggtcttt	1800										
348	ggtatgggcc	ttcttgaggg	caacaagatg	tcatcctcca	agggcaacgt	catactcctg	1860										
350	agggatgcca	tcgagaagca	cggtgcagac	gtggtgccgc	tcttcctcat	gtcctcagca	1920										
352	gagccatggc	aggacttga	ctggagggag	agtgaggtca	tcgggacccg	caggaggatt	1980										
354	gaatggttca	ggaaattcgg	agagagggtc	tcaggtatcc	tggatggtag	gccagtcctc	2040										
356	agtgaggttta	ctccagctga	acctgaaagc	ttcattggaa	ggtggatgtat	gggtcagctg	2100										
358	aaccagagga	tacgtgaagc	cacaaggccc	cttgaatcat	tccagacaag	aaaggcagtt	2160										
360	caggaggcac	tctatctcct	aaaaaggat	gttggaccact	accttaagcg	tgttgagggt	2220										
362	agagttgatg	atgaggttaa	atctgtcctt	gcaaaacgttc	tgcacgcctg	gataaggctc	2280										
364	atggctccat	tcatacccta	cactgctgag	gagatgtggg	agaggtatgg	tgttgagggt	2340										
366	ttttagcag	aagctccatg	gcctgacttc	tcagatgtat	cagagagcag	ggatgtgcag	2400										
368	gttgcagagg	agatggtcca	gaataccgtt	agagacattc	aggaaatcat	gaagatcctt	2460										
370	ggatccaccc	cggagagggt	ccacatatac	acctcaccaa	aatggaaatg	ggatgtgcta	2520										
372	agggtcgcag	cagaggttagg	aaaactagat	atgggctcca	taatggaaag	ggtttcagct	2580										
374	gagggcatcc	atgataacat	gaaggagggtt	gctgaatttg	taaggaggat	catcagggac	2640										
376	cttggtaaat	cagaggttac	ggtgatagac	gagtagacgc	tactcatgga	tgcacatgtat	2700										
378	tacattgaat	cagaggttgg	agccagggtt	gtgatacaca	gcaaaccaga	ctatgaccct	2760										
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384	<211>	LENGTH: 932															
385	<212>	TYPE: PRT															
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391	1					5				10				15			
394	Lys	Asp	Arg	Ile	Phe	Glu	Ser	Asp	Pro	Asn	Glu	Lys	Glu	Lys	Phe	Phe	
395							20			25				30			
398	Leu	Thr	Ile	Pro	Tyr	Pro	Tyr	Leu	Asn	Gly	Asn	Leu	His	Ala	Gly	His	
399							35			40				45			
402	Thr	Arg	Thr	Phe	Thr	Ile	Gly	Asp	Ala	Phe	Ala	Arg	Tyr	Met	Arg	Met	
403						50			55			60					
406	Lys	Gly	Tyr	Asn	Val	Leu	Phe	Pro	Leu	Gly	Phe	His	Val	Thr	Gly	Thr	
407	65					70				75				80			
410	Pro	Ile	Ile	Gly	Leu	Ala	Glu	Leu	Ile	Ala	Lys	Arg	Asp	Glu	Arg	Thr	
411						85				90				95			
414	Ile	Glu	Val	Tyr	Thr	Lys	Tyr	His	Asp	Val	Pro	Leu	Glu	Asp	Leu	Leu	
415						100			105					110			
418	Gln	Leu	Thr	Thr	Pro	Glu	Lys	Ile	Val	Glu	Tyr	Phe	Ser	Arg	Glu	Ala	
419						115			120					125			

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; N Pos. 3750,3770
Seq#:18; N Pos. 3749,3769
Seq#:19; N Pos. 3749,3769
Seq#:20; N Pos. 3274,3294
Seq#:72; N Pos. 31,45,77

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,10,12,17,18,19,20,21,23,24,25,26,27,28,29,30,31,32,33,34
Seq#:35,36,72

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:3720
L:1196 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:3720
L:1379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:3720
L:1546 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:3240
L:2260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72 after pos.:0
M:341 Repeated in SeqNo=72